

Figure 1

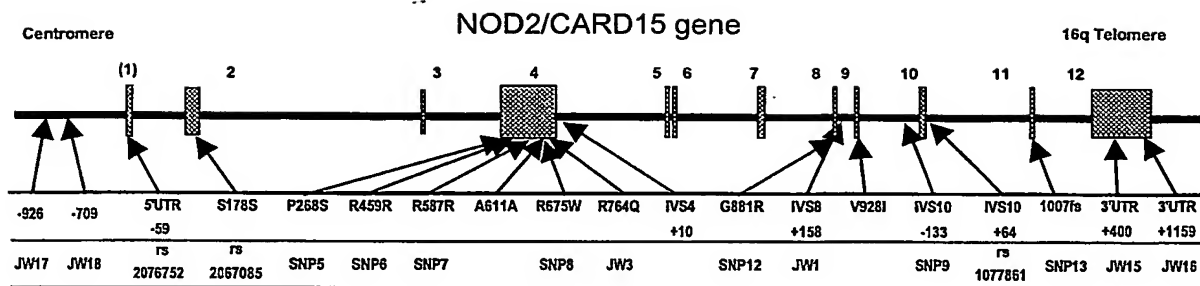
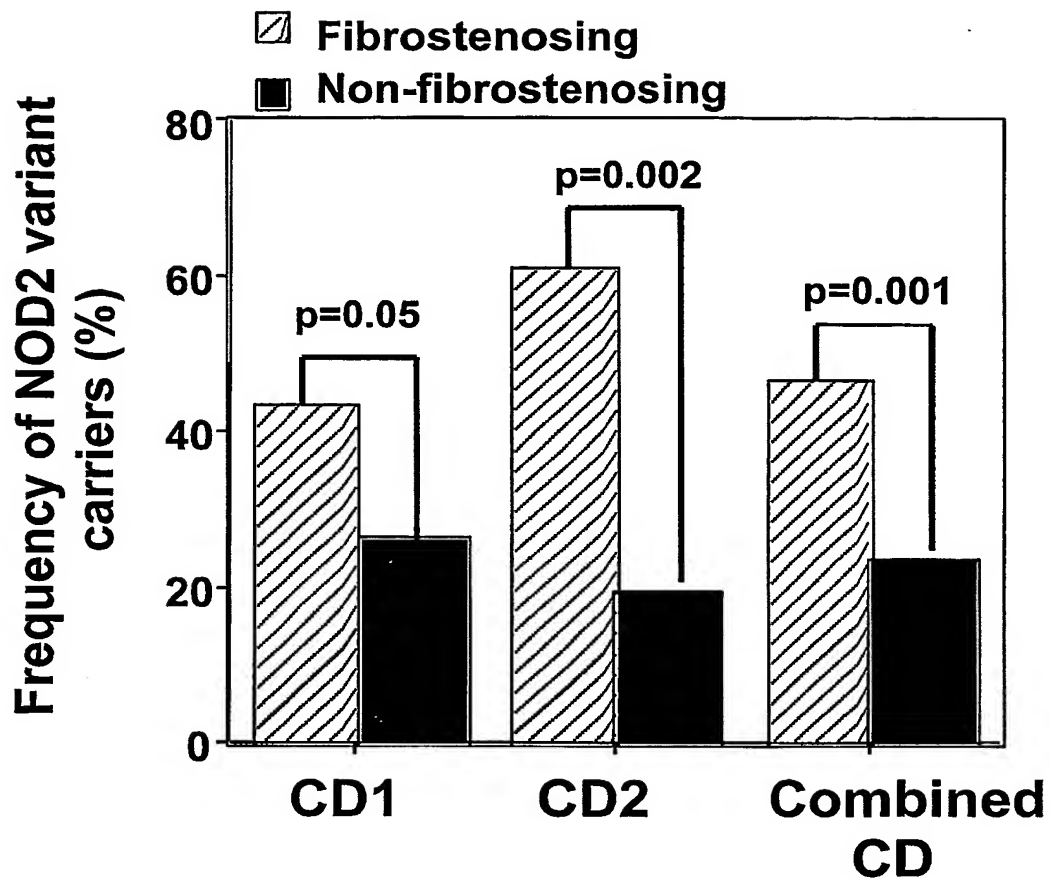
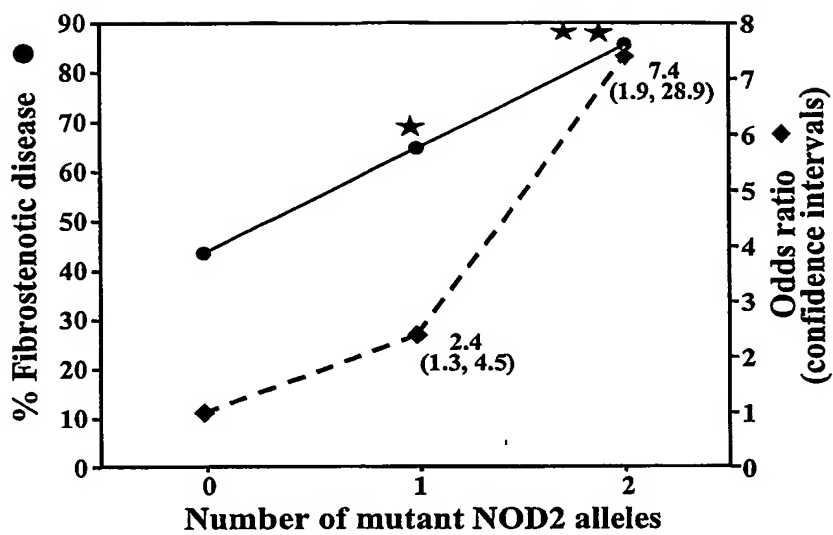


Figure 2



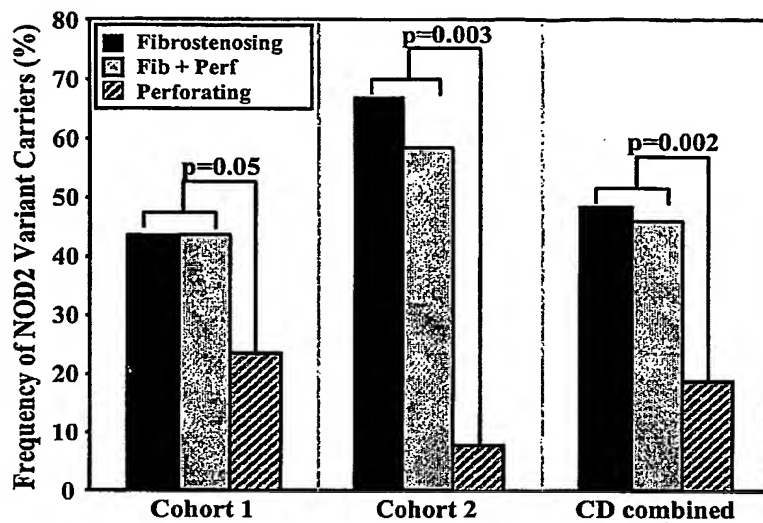
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Figure 3



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Figure 4



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FIGURE 5  
SNP 8

5' ACCCTTCAGT CACAGCGCC TTCTGCGG GGTGTGTGTC CCGGACGAC 50  
 3' TGGAGTCTA GTCTGTCCG AAGCAAGTC CCGCTACAG GGGCTGTGTG  
 TGGGGCTTC TGGCTGAGTC CCGCTACTT CACAGCGCC TGGTCCGCTC 100  
 ACCGCGACG ACCACTCAC GTCTGTAGA CTCTTCGGG ACGAGGCGT  
CGCGCTGTG CCGGCTGGT GTCTGCGCG CAGGCTCCG AAGCTCTTC 150  
CT CCGACAC GCGCGACCA CAGCTCGGC GTGGAGCGG TTGTGAGG  
 ACTCCATCC CCGACTGCA CCGGTGAGG CCGAGAGGT GCATGCCATG 200  
TCAGGTAGCG CCGTCCAGT GCGCACTCC GGTCTCGCA CGTACGTAC  
 CCGCGTTCA TCTGGCTCAT CCGAGCGTG TAGGAGATC AGGAGGAGG 250  
 GCGCCCAAGT AGCCCGATA GCGTGGAC ATGCTCTAG TCTCTCTGC  
 CCGGCTCCG AAGCTGCAC GTGGCTGTA TGTGGGCAC CTCAGTTCA 300  
 CCGCCGACC TTGGAGGTG CACCGCACTT ACAACCGTG CAGTTCAACT  
 CATTGTGCG TGTGGGCCCC ACTGAGTGT CTGCGCTGGC CTTTGTGCTG 350  
 GTAAACGTC ACGCCGGGG TCACTGCG CCGGGACCG GAACACGAC  
 CAGCACTTC GCGGCGCGGT GCGCTGCG CTGGCTTCA ACTCTGTGG 400  
 GTGTGGAGG CCGCGCGCA CCGCGAGTC CAGCTGATG TGAACACCC  
 TCACATGCG GTGGAGTAC TCTGCGTTG CCGTGGTGT TCGAGGCTC 450  
 ACTGTACCG CACCTGTGC ACGACCAAC GCAACGACG ACCTTCCTG  
 TGTGTGAGT GTTACTCGG ATTCTGTTC AGGTATCGG CAGC 3' SEQ ID NO 1 494  
 ACATCACTCA CATTGACCG TAACGACG TCCATACCC CTCG 5' SEQ ID NO 2

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Figure 6

## SNP 12

5' ATCAAAACCC TGAGAGGACA AGGCACATTT CCAAGTCACC CAGAAAGACT 50  
 3' TAGTTTTGGG ACTCTCTGT TCCCTGTAAA GGTTCAGTGG GTCTTTCTGA  
  
 CGAGTGTCTT CTCTTGAAT CCAATGGTCT TTTTTCCTTA CTCCATTGCC 100  
 GCTCACAGGA GAGAACTTTA GGTACCAGA AAAAAGGAAT GAGGTAACGG  
  
 TAACATTGTG GGGTAGAAAT AAAGTTCAA GACCTTCAGA ACTGGCCCCA 150  
 ATTGTAACAC CCCATCTTTA TTTCAAGTTT CTGGAAGTCT TGACCGGGGT  
  
 GCTCTCTCTT CTTCACCTGA TCTCCCCAAG AAAACTGCAG GATAGACTCT 200  
 CGAGGAGGGA GAAGTGGACT AGAGGGGTTC TTTTCACGTC CTATCTGAGA  
  
 GAAGCTTACC TGAGCCACCT CAAGCTCTGG TGATCAGCCA AGGCTTCAGC 250  
 CTTCGAATGG ACTCGGTGGA GTTCGAGACC ACTAGTGGGT TCGAAGTGG  
  
 CAGGGCTTGG GCCCCCTCGT CACCCActct gttgccccag aaTCTGAAAA 300  
 GTCCCGGACC CGGGCGAGCA GTGGGTgaga caacggggtc ttAGACTTTT  
  
 GGCCAAAAGA GTCAACAGAC AGTGTACAGTG AGTACCTGAT ATGTGTTCTA 350  
 CCGGTTTTCT CAGTTGCTCTG TCACAGTCAC TCATGGACTA TACACAAGAT  
  
 GACATGAACT AACAGTCTTC CTCCCTCTGC AGTCCCAGCC AGAGGGGCAG 400  
 CTGTACTTGA TTGTACAGGAG GAGCGAGACG TCAGGGTGGG TCTCCCCGTC  
  
 GACCACTCAA TCCCAGAGTG GCCTCACTGG GGCTCTGGT CCCAGCAAAG 450  
 CTGGTGAGTT AGGGTCTCAC CGCAGTGACC CCGAGGACCA GGGTCGTTTC  
  
 TGGACCTGCC TCCATCTTTT GGGTGGGATG GCCAAACTTA ACCCAAGAGT 500  
 AACTGGAOCC AGGTAGAAAA CCCACCCTAC CCGTTTGAAT TGGGTCTCTA  
  
 TTTTCAGTGGC TTTACATTAC AGACTTAGAG AATAGTAGAG 3'-SEQ ID NO 3 540  
 AAAGTCACCG AAATGTAATG TCTGAATCTC TTATCATCTC 5'-SEQ ID NO 4

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FIGURE 7

## SNP 13

5' TTTAAAAATG AATCATTGC TCCCTACTTA AACAGGTAAA CACTTCTTTC 50  
 3' AAATTTTTC TTTAGTAACG AGGGATGAAT TTCTCCATTT CTGAAGAAAG  
  
 TTGACACAG AATCAGATCC TTCACATGCA GAATCATTCT CACTGAATGT 100  
 AATCTGTCTC TTAGTCTAGG AAGTGTACGT CTTAGTAACA GTGACTTACA  
  
 CAGAATCAGA AGGGATCCTC AAAATTCTGC CATTCCTCTC TCCCGTCACC 150  
 GICTTAGTCT TCCCTAGGAG TTTTAAGACG GTAAGGACAG AGGCCAGTGC  
  
 CCATTTTACA CATAGAAAA CTGAGGTTCG GAGAGCTAAA ACAGGCCTGC 200  
 GGTAAAAATGT CTATCTTTT GACTCCAACC CTCCTGATTT TGTCGGGACG  
  
 CCAGGGCCCT TACCAGACTT CCAGGATGGT GTCATT cctt tcaagggggcc 250  
 GGTCCTCCGA ATGGTCTGAA GGTCCTACCA CAGTAaggaa agttccccgg  
  
 tgc AGGAGCG CTTCCTGCCCC TAGGTAGGIG ATGCAGTTAT TGGACAACCT 300  
 agtTCCTOCC GAAGACGGGG ATCCATCCAC TACGTCAATA ACCTGTTGGA  
  
 GGAAAAGAAG ATACAATGGT GAGCTTCAAG GATTCTTGGT TTCTCTCTTG 350  
 CCTTTTCTTC TATGTTACCA CTCGAAGTTC CTAAGAACCA AAAGGAGAAC  
  
 AAACGTGTCCA GTTAAAGAGA CTGCAGGAGT TACCCAGTCT ACTGAAGCCC 400  
 TTTGACAGGT CAATTTCTCT CAGTCTCTCA ATCGGTGAGA TGAATTGGG  
  
 ACCTGTCCCT TAGACACATC CTGCTCATGT CTGAGATTCC CAATGAGCTC 450  
 TGGACAGCGA ATCTGTGTAG CACGAGTACA GACTCTAAGG GTTACTCGAG  
  
 ATCAACAAAG GCTCAGTACC ATCAGTGAAA TGTAACCGTC TCTCTTCCAT 500  
 TAGTTGTTTC CCAGTCATGG TAGTCACTTT ACATTGGCAG AGACAAGGTA  
  
 TCACTACATG AGTTTATCAA ATTAAGTAGC CACTCCCTTA G3'-SEQ ID NO 5 541  
 AGTGATCTAC TCAATAGTT TAATTCATCG GTGAGGGAAT C5'-SEQ ID NO 6

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FIGURE 8

SNP 5

5' AACAGCAGTG CTCAAAGAGT ACAGTCCGCA CAGCAGGTGG TTTCGCCATC 50  
 3' TTGTCGTAC GAGTTTCTCA TCTCAGCCGT GTCTCTCACC AAACCGGTAC  
  
 CACTGCAGCT GCGCGCAGCT GAATGGGAAG ACAAGAGAA ATTCTGCAA 100  
 GTGACGTCCA CGGCGGTCCA CTTACCCCTC TGTTTCTCTT TAAGCACTTT  
  
 GTCTTGGCCCT GCAGCCCACT GCAAGTGCAG CCGCTGCAGG AGCGTGGCTCT 150  
 CAGAAGCGCA CGTGGGGTGT CGTTCACGTC GCGCAGGTCC TCGCAGGAGA  
  
 TGGCACTGCC CGGCTCAGCC ACCACCAGCA CAGTGTCCGC ATCGTCATTG 200  
 ACGGTGACCG GCGGAGTGGG TGGTGGTGGT GTACACGGCG TAGCAGTAAC  
  
 AGGTGGGAG GGGTGGTGA CAGCTCTCC AGGCCAGGG TGGCTGGGCT 250  
 TCCACCGGTC CCCACGACTT CTCCAGGAGG TCCGGGTCCC ACCGACCGCA  
  
 CTCTGGGGG ggtccagcca tgccacatc TGGCCAGACC TCCAGGACAT 300  
 CAGACGGGC cgaggtcggg acgggtgtag ACCGGTCTGG AGGTCTGTGA  
  
 TCTCTGTGA TATGTCTCC AGGCAGACCG TCTCTGCTCC ATCATAGGTA 350  
 AGACACACAT ATACAGGAGG TCCGTCTCC AGACAGGAG TAGTATCCAT  
  
 CAGAGGAAGC GAGACTGAGC AGACACCGTG GTCTCAGCT TGGCCATATA 400  
 GACTCTTCC CTCTGACTCC TCTGTGGCAC CAGGAGTCCA ACCGGTATAT  
  
 CTCTTTCAT GTGGCAGCTG CAGGCAGAA CAGCAGGAG ATGAAGGTGG 450  
 CAGACAGTA CACCGTCAC CTTCGGTCTT CTCTCCGTC TACTTCACC  
  
 CACCATGGTG APCACGGAC CTAACCAGAC AATGGGCTGC TCGCGGGAC 500  
 GTGGTACCAC TTCTGCGCTG GATGGTCTG TTACCGAGC AGGCCCCCTG  
  
 GCTGACATAA CTCAGGGAT AGCAGGCA GCGGCGGCG3'-SEQ ID NO 7 540  
 CGACTGTATT CACTTCCCTA TCTCTCGGT CGGCGGGG5'-SEQ ID NO 8

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FIGURE 9

JW1

5' CCAC TGGGCA CCCACTACCA ATCGATTGCA ATTGGTCCCTT AAGATAAAAT 50  
 3' CGTGACCCGT GGGTCATCGT TACCTAACCT TAACCAGGAA TTCTATTTTA  
  
 GTACCTGATC CAGCCCAATA TCTTCAATTT ACAGATACTG TATCAAAACC 100  
 CATGGACTAG GTCCGGTTAT AGAAGTTAAA TGTCTATGAC ATAGTTTTGG  
  
 CTGAGAGGAC AAGGGACATT TOCAAGTAC CCAGT agac tccagtggtcc 150  
 GACTCTCTG TTCCCTGTAA AGGTTGAGTG GGTCttctg agctcacagg  
  
TCTCTTCAAA TCCAATGGTC TTTTTTCCCTT ACTCCATTGC CTAACATTGT 200  
ACAGACTTT AGGTTACCAG AAAAAAGGAA TGAGGTAAAG GATTGTAAAC  
  
 GCGGTAGAAA TAAAGTTCAA AGACCTTCAG AACTGGCCCC AGCTCTCTCC 250  
 CCCATCTTT ATTTCAGTT TCTGGAAGTC TTGACCGGGG TCGAGCAGGG  
  
 TCTTCACCTG ATCTCCCCAA GAAACTGCA GGATAGACTC TGAAGCTTAC 300  
 AGAAGTGCAC TAGAGGGGTT CTTTGTAGCT CCTATCTGAG ACTTGAATG  
  
 CTGAGCCACC TCAAGCTCTG GTGATCAGCC AAGGCTTCAG CCAGGGCCTG 350  
 GACTCGGTGG AGTTGAGAC CACTAGTGGG TTCCCAAGTC GGTCCTCGAC  
  
 GGCCCCCTCG TCACCCACTC TGTTCGCCCCA GAATCTGAAA AGGCCAAAAG 400  
 CCGGGGGACC AGTGGGTGAG ACAACGGGGT CTTAGACTTT TCCGGTTTTT  
  
 AGTCAACAGA CAGTGTGAGT GAGTACCTGA TATGTGTCT AGACATGAAC 450  
 TCAGTTGTCT GTCACAGTCA CTCATGGACT ATACACAAGA TCTGTACTTG  
  
 TAACAGTCTT CCTCCCTCTG CAGTCCCACC CAGAGGGGCA GGACCACTCA 500  
 ATTGTACGA GAGGGCAGAC GTCAGGGTCG GTCTCCCCGT CCTGGTCACT  
  
 ATCCCAGAGT GGCTCACTG 3'-SEQ ID NO 9 520  
 TAGGGTCTCA CCGAGTGAC 5'-SEQ ID NO 10

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SEQ ID NO:12	01SS7	1	-----AATCAATTAATGCTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	61
SEQ ID NO:13	02SS7	1	-----TCTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	53
SEQ ID NO:14	03SS6	1	-----TTATGCTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	56
SEQ ID NO:15	04SS7	1	-----TTATGCTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	56
SEQ ID NO:16	05SS7	1	-----TTATGCTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	56
SEQ ID NO:17	06SS2	1	-----TTATGCTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	56
SEQ ID NO:18	08SS7	1	-----TCTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	52
SEQ ID NO:19	12SS7	1	-----TCTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	51
SEQ ID NO:20	13SS7	1	-----TAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	49
SEQ ID NO:21	14SS7	1	-----CTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	50
SEQ ID NO:22	19SS7	1	-----TCTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	53
SEQ ID NO:23	22SS7	1	-----TCTAGCTTCAGTTTCTCTGCTTTCAGTTTAAATTTGGAAAGAGAGAGAGAAA	53

JW18

00STD	101	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	200
01SS7	62	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	161
02SS7	54	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	153
03SS6	57	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	156
04SS7	57	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	156
05SS7	57	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	156
06SS2	57	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	156
08SS7	53	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	152
12SS7	52	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	151
13SS7	51	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	149
14SS7	51	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	150
19SS7	54	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	153
22SS7	54	AATATCACTGATTAATCTGTTTCTTAAATTTGCTCTTAACATCTTCTCTTATTAATTAATCTGCTGGGCTTCCCTCTTCAGGCGAAATCTGTC	153

00STD	201	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	300
01SS7	162	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	261
02SS7	154	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	253
03SS6	157	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	256
04SS7	157	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	256
05SS7	157	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	256
06SS2	157	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	256
08SS7	153	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	252
12SS7	152	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	251
13SS7	150	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	249
14SS7	151	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	250
19SS7	154	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	253
22SS7	154	AGCTATCTGCATGCTTTTGAATCTCTACTTCACTTACAACTTCAAGACACCATTTGCTCTCCCAAGGTGAGGCGCCATGTAGAGAAAGGATCACT	253

FIGURE 10

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009TD	301	TCCTTGTCTGAAGAGAGGGGTCAAGGGG	353	TCCTTGTCTGAAGAGAGGGGTCAAGGGG
019S7	262	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	400	
029S7	254	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	361	
039S7	257	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	353	
049S7	257	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	356	
059S7	257	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	356	
069S7	257	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	356	
079S7	253	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	352	
129S7	252	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	351	
139S7	250	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	349	
149S7	251	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	350	
159S7	254	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	353	
229S7	254	GA CCCACGTGGGCCCCCTCCCTGAAACCCAGGCCAGGCTGAGCTTGACACCTCTCTCTCTCTGAGACCCAC	353	

009TD	401	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	500	GGAGAGGGAGGGGAGGCCCA
019S7	362	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	461	GGAGAGGGAGGGGAGGCCCA
029S7	354	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	453	GGAGAGGGAGGGGAGGCCCA
039S7	357	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	456	GGAGAGGGAGGGGAGGCCCA
049S7	357	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	456	GGAGAGGGAGGGGAGGCCCA
059S7	357	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	456	GGAGAGGGAGGGGAGGCCCA
069S7	353	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	452	GGAGAGGGAGGGGAGGCCCA
129S7	352	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	451	GGAGAGGGAGGGGAGGCCCA
139S7	350	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	449	GGAGAGGGAGGGGAGGCCCA
149S7	351	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	450	GGAGAGGGAGGGGAGGCCCA
159S7	354	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	453	GGAGAGGGAGGGGAGGCCCA
229S7	354	AGCCAGCCCGGTTTCTCTGGGGCCCAAGAGCAATGCTTTGCTTAAAGTCTGAAATCTCAGCCCACTGACCCCTTGACAC	453	GGAGAGGGAGGGGAGGCCCA

FIGURE 10 (continued)

009TD	501	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	535
019S7	462	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	496
029S7	454	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	488
039S7	457	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	491
049S7	457	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	491
059S7	457	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	491
069S7	457	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	491
079S7	453	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	487
129S7	452	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	486
139S7	450	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	484
149S7	451	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	485
159S7	454	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	488
229S7	454	GGGAAGCTCAACTTCCCAAGTGTCTGAGTCTCTG	488

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SEQ ID NO:24	00STD	1	TCACATGCTCTGGTTCATGCTGTAACCTGAACTGCTGCAACACAGACCTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	100
SEQ ID NO:25	01SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	63
SEQ ID NO:26	02SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	65
SEQ ID NO:27	03SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	62
SEQ ID NO:28	04SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	70
SEQ ID NO:29	05SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	70
SEQ ID NO:30	06SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	69
SEQ ID NO:31	08SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	63
SEQ ID NO:32	12SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	70
SEQ ID NO:33	13SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	63
SEQ ID NO:34	14SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	65
SEQ ID NO:35	19SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	66
SEQ ID NO:36	22SS6	1	-----TGACACACAGACTTCGAAATAGACCCCAAGAGGCGAGTCCATTTTCATTTTGGCCAGAAATGCT	200
SEQ ID NO:37	00STD	101	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	163
SEQ ID NO:38	01SS6	64	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	163
SEQ ID NO:39	02SS6	66	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	165
SEQ ID NO:40	03SS6	63	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	162
SEQ ID NO:41	04SS6	71	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	170
SEQ ID NO:42	05SS6	71	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	169
SEQ ID NO:43	06SS6	70	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	169
SEQ ID NO:44	08SS6	70	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	163
SEQ ID NO:45	12SS6	64	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	170
SEQ ID NO:46	13SS6	71	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	163
SEQ ID NO:47	14SS6	64	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	163
SEQ ID NO:48	19SS6	66	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	165
SEQ ID NO:49	22SS6	67	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	166
SEQ ID NO:50	00STD	201	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	300
SEQ ID NO:51	01SS6	164	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	263
SEQ ID NO:52	02SS6	166	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	265
SEQ ID NO:53	03SS6	163	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	262
SEQ ID NO:54	04SS6	171	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	270
SEQ ID NO:55	05SS6	171	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	270
SEQ ID NO:56	06SS6	170	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	269
SEQ ID NO:57	08SS6	170	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	269
SEQ ID NO:58	12SS6	164	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	263
SEQ ID NO:59	13SS6	171	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	270
SEQ ID NO:60	14SS6	164	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	263
SEQ ID NO:61	19SS6	166	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	265
SEQ ID NO:62	22SS6	167	TTAGGATGTACAGTTATGATTCAGGAAATTTAGGCGCTTCCTTCAAGACCAATAGTCTTCTCGGATTAATTCAAAATGATGTATGTTG	266

FIGURE 11A

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FIGURE 11A (continued)

SEQ ID NO:55	00STD	1	TTGGCTCTCAGTTGTTGTCAGAGGCTGTGAGTTT	100
SEQ ID NO:56	01896	1	-----	54
SEQ ID NO:57	02886	1	-----	64
SEQ ID NO:58	03896	1	-----	64
SEQ ID NO:59	04886	1	-----	50
SEQ ID NO:60	05882	1	-----	57
SEQ ID NO:61	06896	1	-----	66
SEQ ID NO:62	08896	1	-----	65
SEQ ID NO:63	12886	1	-----	65
SEQ ID NO:64	13886	1	-----	65
SEQ ID NO:65	14886	1	-----	70
SEQ ID NO:66	19886	1	-----	20
SEQ ID NO:67	22886	1	-----	67
00STD	101		-----	200
01896	65		-----	164
02886	65		-----	164
03896	65		-----	164
04896	51		-----	150
05882	68		-----	167
06886	67		-----	166
08886	66		-----	165
12886	66		-----	165
13886	66		-----	165
14886	71		-----	170
19886	21		-----	120
22886	68		-----	167
00STD	201		-----	300
01886	165		-----	264
02886	165		-----	264
03886	165		-----	264
04886	151		-----	250
05882	168		-----	267
06886	167		-----	266
08886	166		-----	265
12886	166		-----	265
13886	166		-----	265
14886	171		-----	270
19886	121		-----	220
22886	168		-----	267

FIGURE 11B

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DNA ID	301	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	400	
	009TD	301	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	400
	01896	265	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	364
	02896	265	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	364
	03896	265	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	364
	04886	251	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	350
	05892	268	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	367
	06886	267	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	366
	08886	266	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	365
	12886	266	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	365
	13886	266	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	365
	14886	271	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	370
	19886	221	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	320
	22886	268	GGGTCACTGGGGCCCATGATGCTGTGTTAACTGAGTGCCCTTTTGGTGAGAGAGCCCGGCTCTCTCAAAAGAGCCCTTTTCCACTGCTCTGATGAAGAG	367
	009TD	401	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	500
	01896	365	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	464
	02896	365	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	464
	03896	365	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	464
	04886	351	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	450
	05882	368	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	467
	06886	367	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	466
	08886	366	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	465
	12886	366	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	465
	13886	366	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	465
	14886	371	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	470
	19886	321	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	420
	22886	368	GAGTACACAGAACACATAATTTCAGGAAGGAGCTTTTCCCATGCTCGACTCATCCATCCAGGCCATTTCCCGTCTCTGGTTCTTCCCTCCTCTGGACT	467
	009TD	501	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	533
	01896	465	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	497
	02886	465	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	497
	03886	465	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	497
	04886	451	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	483
	05882	468	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	500
	06886	467	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	499
	08886	466	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	498
	12886	466	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	498
	13886	466	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	498
	14886	471	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	503
	19886	421	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	453
	22886	468	CTTGACACAGCTCCTCTCTGAGGCTGAAATT	500

FIGURE 11B (continued)

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